AMENDMENT TO THE SPECIFICATION:

Please amend paragraph [1] at page 1 of the application as follows:

[01] This application is a continuation of and claims the benefit of U.S. Provisional Application No. ~~60/~~ 60/221,611 , by Doyle et al. entitled, METHOD AND SYSTEM FOR THE MULTIDIMENSIONAL MORPHOLOGICAL RECONSTRUCTION OF GENOME EXPRESSION ACTIVITY filed July 28, 2000, the disclosure of which is incorporated herein by reference.

Please amend paragraph [6] at pages 1 and 2 of the application as follows:

[06] Craig Venter, a former NIH researcher, advocated taking a different approach. His idea was rather to take the approach of splitting up the entire genome into small fragments and working on them en masse. This involved dividing the sequencing task among many automatic sequencing machines and attacking the task in parallel, with large numbers of short sequences being determined, and then proceeding to process more batches of the short fragments. Computer scientists then proceeded to reconstruct the fragments' proper order using algorithmic overlap-analysis methods first proposed by Leroy Hood. This method became called "shotgun sequencing" and although persistently derided by the established authorities in the HGP, it proved to be extremely effective in making rapid progress toward the goal of sequencing an entire genome. This work led to the joint announcement on June 26, 2000 by Craig J. Venter, president of Celera Genomics ~~(http://www.celera.com),~~ and National Human Genome Research Institute director Francis S. Collins of completion of "the first survey of the entire human genome." The "survey" is the "working draft" of the human genome produced by the publicly funded international consortium HGP and the "first assembly of the human genome" produced by privately funded Celera Genomics.

Please amend paragraph [15] at pages 3 and 4 of the application as follows:

[15] Since the gene expression activity of organs and tissues can be quite complex, it is desirable to use a technique which allows analysis of the gene expression, but which permits the morphologic localization of the area to be studied, thus avoiding the loss of morphological detail that results from the homogenization process. Laser capture microdissection (LCM) allows this to be done with great specificity [Bonner, R.F., et al., Science, 278(5342):1481, 1483 (1997); Cole, K.A. et al., Nat Genet, 21(1 Suppl):38-41 (1999); Emmert-Buck, M.R., et al., Science, 274(5289):998-1001 (1996)] ~~(http:/meeko.niehd.nih.gov/lcm/lcm.htm)~~.